## We claim:

- 1. A method of identifying one of a plurality of preselected polymorphisms that may be present in a cytochrome P450 2D6 gene sequence in a sample, the method comprising:
  - (a) incubating a reaction comprising:
  - (i) an amount of nucleic acid obtained from said sample sufficient for primer extension, wherein said nucleic acid comprises said P450 2D6 gene sequence,
    - (ii) a nucleic acid polymerase,
    - (iii) a plurality of extension primers that specifically bind to a P450 2D6 gene sequence, and that, when extended by one nucleotide at the 3' end, comprise a nucleotide indicative of one of a plurality of preselected polymorphisms in said P450 2D6 gene sequence, and
      - (iv) a set of distinctively labeled ddNTPs,

under conditions such that at least one of said extension primers is distinctively labeled by addition of one of said ddNTPs comprising a label to the 5'-end of said detection primer, to generate at least one labeled nucleic acid corresponding to at least one of said preselected polymorphisms; and

- (b) relating the labeled nucleic acid to the identity of said polymorphism in said sample.
- 2. The method of claim 1, wherein said nucleic acid is obtained from said sample by amplification of DNA in said sample.
- 3. The method of claim 2, wherein said amplification is accomplished by the addition of nucleic acid primers having SEQ ID NOs 1 to 8.
- 4. The method of claim 1, wherein said relating step (b) comprises mobilizing said labeled nucleic acid(s) by electrophoresis.

60

DLMR238518.1

- 5. The method of claim 4, wherein said electrophoresis is capillary electrophoresis.
- 6. The method claim 1, wherein one or more of steps (a), (b) or (c), or combinations thereof, are automated.
- 7. The method of claim 1, wherein said distinctive labeled ddNTPs are fluorescently labeled.
- 8. The method of claim 1, wherein said plurality of preselected cytochrome P450 2D6 polymorphisms are independently selected from the group consisting of a duplication, a deletion, an inversion, an insertion, a translocation, a polymorphism resulting in aberrant RNA splicing, and a single nucleotide polymorphism.
- 9. The method of claim 1, wherein said preselected cytochrome P450 2D6 polymorphisms are selected from the group consisting of CYP2D6\*3, CYP2D6\*4, CYP2D6\*5, CYP2D6\*6, CYP2D6\*7, CYP2D6\*8, CYP2D6\*10, CYP2D6\*17 and CYP2D6\*Nx2.
- 10. The method of claim 9, wherein said extension primers have sequences selected from the group consisting of SEQ ID NOS: 9 through 19.
  - 11. The method of claim 1, wherein said sample is a human sample.
- 12. The method of claim 1, wherein said polymorphism is associated with phenotype selected from the group consisting of having a reduced rate or degree of metabolism of one or more xenobiotics or endobiotics, an increased rate or degree of metabolism of one or more xenobiotics or endobiotics, a decreased or increased specificity for one or more xenobiotics or endobiotics, and combinations thereof.
- 13. The method of claim 12, wherein said xenobiotic is a toxin, a carcinogen or a narcotic, or a metabolic precursor thereof.
- 14. The method of claim 13, wherein said sample is a sample from a subject having a genetic predisposition to suffer from a toxin, a carcinogen, or a narcotic.

- 15. The method of claim 12, wherein said xenobiotic is a therapeutic drug or a metabolic precursor thereof.
- 16. The method of claim 15, wherein said therapeutic drug is a cardioactive drug or a psychoactive drug.
- 17. The method of claim 15, wherein said subject has a disease or disorder that may be treated by said therapeutic drug.
  - 18. The method of claim 1 further comprising detection of wildtype P450 2D6.
- 19. A method of identifying a polymorphism in a cytochrome P450 2D6 gene sequence in a sample, the method comprising:

generating from said sample a labeled nucleic acid comprising a means for distinguishing amongst a plurality of preselected polymorphisms in said P450 2D6 gene; and

relating said labeled nucleic acid to the identity of said polymorphism in said sample.

- 20. The method of claim 19, wherein said nucleic acid is obtained from said sample by amplification of DNA in said sample.
- 21. The method of claim 20, wherein said amplification is accomplished by the addition of nucleic acid primers having SEQ ID NOs 1 to 8.
- 22. The method of claim 19, wherein said means for distinguishing amongst a plurality of preselected polymorphisms comprises a primer extension reaction with distinctively labeled ddNTPs and size separation of labeled primers by electrophoresis.
  - 23. The method of claim 22, wherein said electrophoresis is capillary electrophoresis.
- 24. The method claim 19, wherein said means for distinguishing amongst a plurality of preselected polymorphisms is automated.
- 25. The method of claim 22, wherein said distinctively labeled ddNTPs are fluorescently labeled.

- 26. The method of claim 19, wherein said plurality of preselected cytochrome P450 2D6 polymorphisms are independently selected from the group consisting of a duplication, a deletion, an inversion, an insertion, a translocation, a polymorphism resulting in aberrant RNA splicing, and a single nucleotide polymorphism.
- 27. The method of claim 19, wherein said preselected cytochrome P450 2D6 polymorphisms are selected from the group consisting of CYP2D6\*3, CYP2D6\*4, CYP2D6\*5, CYP2D6\*6, CYP2D6\*7, CYP2D6\*8, CYP2D6\*10, CYP2D6\*17 and CYP2D6\*Nx2.
- 28. The method of claim 27, wherein said extension primers have sequences selected from the group consisting of SEQ ID NOS: 9 through 19.
  - 29. The method of claim 19, wherein said sample is a human sample.
- 30. A method of selecting a therapeutic drug, or a prodrug thereof, to treat a subject suffering from a disease or disorder, said method comprising:

selecting said therapeutic drug or prodrug to be compatible with a cytochrome P450 2D6 genotype of said subject identified by the method of claim 1 or 19.

31. A method of selecting a dosage of a therapeutic drug, or a prodrug thereof, to treat a subject suffering from a disease or disorder, said method comprising:

selecting said dosage to be compatible with a cytochrome P450 2D6 genotype of said subject identified by the method of claim 1 or 19.

- 32. The method of claim 31 or 32, wherein said P450 2D6 genotype of said subject comprises a cytochrome P450 2D6 gene selected from the group consisting of CYP2D6\*3, CYP2D6\*4, CYP2D6\*5, CYP2D6\*6, CYP2D6\*7, CYP2D6\*8, CYP2D6\*10, CYP2D6\*17 and CYP2D6\*Nx2.
- 33. A substantially purified nucleic acid that hybridizes to the P450 2D6 gene, said nucleic acid selected from the group consisting of SEQ ID NOs 9 to 19.

- 34. The substantially purified nucleic acid of claim 33 wherein said nucleic acid is SEQ ID NO:11.
- 35. The substantially purified nucleic acid of claim 33 wherein said nucleic acid is SEQ ID NO:14.
- 36. A method of identifying at least one of a preselected polymorphism that may be present in a cytochrome P450 2D6 gene sequence in a human sample, the method comprising:
  - (a) incubating a reaction comprising:
  - (i) an amount of nucleic acid obtained from said sample sufficient for primer extension, wherein said nucleic acid comprises said P450 2D6 gene sequence,
    - (ii) a nucleic acid polymerase,
    - (iii) at least one extension primer selected from the group consisting of SEQ ID NOs 9 to 19, and
      - (iv) a set of distinctively labeled ddNTPs,

under conditions such that said at least one extension primer is distinctively labeled by addition of one of said ddNTPs comprising a label to the 5'-end of said at least one detection primer, to generate at least one labeled nucleic acid corresponding to at least one of said preselected polymorphisms; and

- (b) relating the labeled nucleic acid to the identity of said polymorphism in said sample.
- 37. The method of claim 36, wherein said nucleic acid is obtained from said sample by amplification of DNA in said sample.
- 38. The method of claim 37, wherein said amplification is accomplished by the addition of nucleic acid primers having SEQ ID NOs 1 to 8.

- 39. The method of claim 36, wherein said relating step (b) comprises mobilizing said labeled nucleic acid(s) by electrophoresis.
  - 40. The method of claim 39, wherein said electrophoresis is capillary electrophoresis.
- 41. The method claim 36, wherein one or more of steps (a), (b) or (c), or combinations thereof, are automated.
- 42. The method of claim 36, wherein said distinctive labeled ddNTPs are fluorescently labeled.
  - 43. The method of claim 36, wherein said primers are SEQ ID NO: 17, 18 and 19.
  - 44. The method of claim 36, wherein said primers are SEQ ID NO: 11.
  - 45. The method of claim 36, wherein said primers are SEQ ID NO: 11 ND 14.